Atty. Docket No.: 077319-0382

Trp

GGAAGTCAGCAGGCGTTGGGGAGGGGTGGCGGGGGAATAGCGGCGGCAGC

Figure

CCA GGG GCA TGG CCGCTGCCGCAGCCTGGCGAGGGGGCCAGCCCCCAGGCCCCTAC GGGGACAGCCCCCCACCATTCCTACCGCTATGGGCCCCAACCTCCCACTCC CACCTCCCTCCATCGGCCGGGCTAGGACACCCCCAAATCCCGTCGCCC CCTTGGCACCGACACAGAGACAGAGACAGACACAGCCATCCGCCACCA Gly Ala Pro Trp TGG Asp Leu TTG GAT Met ATG CCCTCTGAGGTGGCCAGA

151

101

201

251

301

20 Н CTG CTC TTC C Phe Leu Leu Phe Leu Leu Leu CLGCIG TTC CTCLeu Leu CTGCTGren ren CTGMet ATG 343

LysAAG SeraAla CCC AGT GCC Pro Ser AGC CysTGC Phe ACC CTG TGG TTC Pro Thr Leu Trp CCC Len CTGen $\mathbf{I}^{\mathbf{G}}$ 380

ATC TGG Trp SGC G1YAsn AAT TYrTACPhe TTCAla GCC Met AAG ATG LysPhe Phe TTCTYr418

CCC $\mathbf{I}\mathbf{G}\mathbf{I}$ GTGCCTATC SCC GCT GTG CTC CTG 455

GTG

Val Ala Cys Pro Val Ile Leu Ala Val Ala Leu Phe en

50

Arg CGTLeu Ile ATC LysAAG ATG AAC GAG GTCCGA 493

Met

Asn

Glu

Val

Asn

Arg

G1y

Arg

9

CGA 999 TAC CTGTAC CAC ATC AAA CICCIGATG 530

Arg Ile Gly TYrLeu TYrLysIle His Leu Met Leu en

80

Figure

C Ser \mathbf{ICG} Pro CCC Pro CCTPhe TTC His CAC His CAC 90 Ala GCT G1YCGA GGG Arg Val GTG Glu Val 568

Len CIC Ser \mathbf{TCT} Ser AGC Gln CAG His CAC Asn TCC AAC Ser Val GTCVal GTTVal GLL Tyr \mathtt{TAT} Pro CCC ln 605

100

U H Gly Arg CGC 120 CCC Pro CCA Len CTGGTA Glu Val GAG Met ATG Gly Met GGG ATG Leu Leu Asp GAT 643

G1yGCT GGC Ala Trp ${
m TGG}$ Leu 130 CIGLeu CTAGluGAG Arg CGC Lys AAG Ala $\mathcal{C}\mathcal{C}\mathcal{C}$ Ile GTG CCC ATT Pro Val γs 680 GT

Figure 1D

I1eATC TGG CTG GCA GGA GTC Val Gly Trp Leu Ala 140 CysTGC CCC Gly Leu Ala CTG TCT GCC GGG Ala Ser 718

Val TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC Ser I1eThr Gly Asp Ala Arg Lys150 Asp Arg Ile he 755

Gln Thr Leu Leu Thr Gln Asp V GTC GCC CAG ACC CTG CTC ACC CAG GAC G 170 Val Ala Glu GAG $ext{LCL}$ Ser 160 ATG Met 793

GTG TTT CCT GAG GGA ACG AGA AAC CAC Phe Pro Glu Gly Thr Arg Asn His Val AGG GTC TGG Trp Val Arg IG 830

180

Figure 1 E

U 田 TTCPhe CCC Ala GGC G1YCGI Phe Lys Arg AAA $\mathbf{T}\mathbf{T}\mathbf{C}$ 190 CCC Pro CTG Leu ATG Met TCC Ser GGC G1YAAT Asn 898

ATA Ile CCC Pro GTCVal ATT Ile CCC Pro CAG GIT Val Gln $\mathcal{C}\mathcal{C}\mathcal{C}$ Ala CAG 200 Gln GTG Val GCA Ala CLL Leu 1.S 905

C Ö 220 AAG LysAAG LysTGC CysTAC TYYTTCPhe Asp GAC CAA Gln TAC $\mathrm{T}\mathrm{Y}\mathrm{r}$ TCC Ser $^{\mathrm{TCC}}$ Ser ATG Met GIC Val 943

GTG Val CGG Arg GTG Gln Val CAG \mathbf{TGT} CysCAA Gln GGA G1y \mathbf{ICG} Ser ACC Thr TTCPhe CGC Arg CGT Arg AG 980

230

Figure 1F

K G Asp GAT Pro CCA ACA Thr CIGLeu Glu Gly GAA GGG 240 ACG Thr CCC Val Pro GTGPro CCA CCC Pro CTGLeu 1018

TCC ATG Met Ser CAC His CGG Arg GAC AGA GTC Val Asp Arg GCT Leu Ala CTG GCT Ala CCA Pro GTC Val AC 1055

250

U <u>ෆ</u> CCC 270 Arg S S S S S G1yTCC ACT GAT Asp Thr Ser ATC IleGAA Glu CGG Arg TIC Phe GTT Thr Val CTC ACT 260 Leu 1093

999 TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCCATCTTCCTCCC CACACCTACCCAGTGGGCCCTGAAGCAGGGCCAAACCCTCTTCCTT Pro Gly Gly Gly 280 GGT SGC 999 CCTAAG LysAAG Gly Gly Asp Tyr Leu Lys CIG \mathtt{TAT} GGT GGT GAC GI1216 1168

GTCTCCCCTCTCCCCACTTATTCTCCTCTTTGGAATCTTCAACTTCTGAA 1266

Figure 1G

ACAAGGGGAAGCAGACATCAGGTGCTGCACTCACTTCTGCCCCCTGG GGAGTTGGGGAAAGGAACCATGGCTGGAGGGGATAGGAGGGCTTTT TCAGTCTCCACATTTCTGGTTTTTCTGTCCCCATAGTACAGTTCTTCAGTG GACATGACCCCACCCCCCTGCAGCCCTGCTGACCATCTCACCAGAC GCCTGCCCTTGCCCAGATGCCCAGGGTCGTGCACTCTCTGGGATACCAGT TGTAGCCTCCTGTCAGTGGGGGCTGGACCCTTCTAATTCAGAGGTCTCAT TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAGCTGATACCTGAAGCACT ACAAATCCCCCCCCACTCCAAGTCCATGGATTCAATGGACTCATTT TGTCTGTGGGACAGTTGCCTCCCCTCATCTCCAGTGACTCAGCCTACAC CTCTACCCCTCTACCCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGA AAGGGAGGGAACATTCCATCCCCAGTGGAGTCTCTTCCTATGTGGTCTT 1316 GTGAATGTGGATACAGCGCCACTCCTGCCCCCTCTTGGCCCCCATCGATGG ACTCTTGCCTCGGTGCAGTTTCCACTCTTGACCCCCCACCTCCTACTGTCT 1916 1966 1866 1816 1716 1466 1616 1666 1766 1516 1566 1416 1366

Figure 1 H

2016	AATTTATTTCTTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTTCA
2066	TTTCTTCCTGGTGGCATTAGCCACTCCCTGCCTCTCACTCCAGACCTGTT
2116	CCCACAACTGGGGAGGTAGGCTGGGAGCAAAAGGAGGGGGGGG
2166	TTTTGCGTGGTTTTTTTTTATTATTTGGATAACAGCAAAAAAACTG
2216	AAAATAAAGAGAGAGAAAAAAAAA

Figure 2 A

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50 <u>F</u> <u>F</u> KMA G <u>F</u> VTIRP <u>F</u> SKS	100 -YGIRVEVRG MLGLDVK -FGLKVECRK WAGVKVQLHA	150 -VPI-AKREL VTAKKSL TVTV-GKKSL STLAVMKKSS	SVMSEVAQTL LTQDVRVWV-DTLNKGLENV KKNKRALWV-GTIAEVVNHF KKRRISIWM-KTLKWGLQRL KDFPRPFWLA	250 LAVQAQVPIV LAQQGKIPIV AAIAAGVPII SAVSIMRDFV
40 <u>LWFCSPSAKY</u> <u>C</u> ILVCVFGSIY <u>LIVN</u> AIQAVL	90 RLMLLHIKYL ARCFYHVMKL GHMFGRLAPL WLQLVWVVDW	140 VLPGRC IFPPGCT- IVQ-PP ILAQRSGCLG		240 MLPFKRGAFH MLPFKKGAFH -LPFKTGAFH VLIPRTKGEV
30 LL-LLFLLPT AL-AG RL-IITVIYS PLGLLFLLSG	80 GRNVENMKIL GKÖHLAQWIT PRNPKHVATF	130 SSLDLLGMME STLDIFMLGR NNYDMVTASN SDIDWL-IGW	180 IDRKRTGDAI LDRSKRQEAI IDRNNRTKAH LERS-WAKDE	220 230 GST SELT RGLT AKLLAAQEYA ASQGLPAPRN
20 <u>LLL</u> LLF YLRSV <u>L-VVL</u> <u>LYIF</u> <u>PL</u> V <u>LVVL</u>	70 VLAIPVCAVR VIASILCTLICLFS EL	120 -PYVVVSNHQ -PYTMIANHQ -NAIYIANHQ EHALIISNHR	170 WLAGVIE WEMALSGTYE WLTGNLL	
10 MDLWPGAWM- MSV-IGRFLY M MAI	60 FYNGWILFLA FYG G FYRRINRFLA	110 AHHF-PPSQ- VVGE-ENLAK PTDA-ESYG- DEETYRSMGK	160 LWAGSAGLAC KYVPFLG LWIPFFGQLY KFLPVIGWSM	210 -FPEGTRNHN -FPEGTRSYT -FPEGTRSRG LFVEGTRFTP
ਜਜਜਜ	51 51 51	101 101 101 101	151 151 151 151	201 201 201 201 201
Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT

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VPTEGLTPDD VPALADR ISTENLTKDK IGEFAEK IDVSQYGKDQ VRELAAH VIHVRMKRHA MSEMPKSDED	340 350 GDYLKKPGGG G* DTTLPPQREAAGK V* PIGRPVKSLL VTLFWSCLLL	390 400 NEPVPSVSIS NDVNTHNEGS GVMHVFIMFS QAERS	440 450
280 GQCQVRVLPP GCMIVRILKP GLVIVEMLPP MLRILKGQSS	330 REISTDGRGG KEIGYSPAIN AELDKEVAE- ATGTFDEEIR	380 HDKKVNKKIK FTAAGMALVT	430
270 YCKKERRETS VSPKYGVENR INLNRLHN IVPKDSPQPT	320 VRHSMLTV-F VRDQMVDT-L CRSIMEQK-I AKDALLDKHL	370 A <u>L</u> Q Q <u>L</u> LSTWRGVA	420 KKMH*
260 PIVMSSYQDF PVVVSNTSTL PVCVSTTSNK PALYDTTV	310 VSKWCKDIFV	360 <u>AIE</u> YA FGAIEFFKWT	410 <u>sv</u> <u>ssaraarnrv</u>
251 251 251 251	301 301 301 301	351 351 351 351	401 401 401
Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT

Figure 3A

60	120	180	240	300	360	420	. 480	540
GCCGTGTCTG	CGAGTTCTAC	CTCGCTCGTC	CTGGTTCGTG	AGGCTGCAĠ	GATGGGCCTC	CTTCCTGGGG	GCGCTCTAGC	STCAAAGTG
50	110	170		290	350	410	470	530 540
TGGAGCTĢTG GC	eccececeec ce	cceccereec cr		GGGACCCGCG CAGGCTGCAG	TCCTGGACAT GA	GGGAGCTGCT CT	TCAACCGGCA GO	TCAGGGAGAA CCTCAAAGTG
40	100		220 230	280	340	400	450 · 460	520
GGCCGGGCCA 1	GTGCAGCTGA		GAGAACATGA GCATCATCGG	TTCGAGGTGC	CACCAGAGCA	ATCGCCAAGC	CCTCGGGGGC GTCTTCTTCA	GAGCGCATGG
30 TCGGGCGCCG		150 CGCGCTGTGC TTCACGGTGT	210 CCGGACGGTG	270 CGGGCTCCGC	330 CGTCTCCAAC	380 TTCCGGAGCG CTGCGTGCAG		510 CGACCTGGGC
20	80	140	200	260	320	380	440	500
Geceececce	TGCTGTTGCT GCTGCTG	CCCTGTACTG	GCCACGGCGG	AGTACTTTTA	CCTGTGTCAT	TTCCGGAGCG	TCATCATGTA	CAGTGATGGC
10	07	130	190	250	310	370	430	490
GGAGCGAGCT		GCCAAGGTCG	TGCCTGCTGT	CGAAGCTTCA	GAGGCCCGTC	ATGGAGGTCC	CCCGTGGGCC	ACTGCCATGA
		•			•			

Figure 3B

					•			
600	660	720	780	840	890	960	1020	1070 1080
Taagaaggg	CTCTTCCTTC	AGTGCAGGTG	CGTGGACACC	GGAGAACGGG	GACCACGGCA GGGCATGACC	CTCCCGGCTT	AGGAAGCCCC	GCAGGGGCT CAGCTGGACC
590	650	710	770	820 830	890	950	1010	
TGCTGCCTTT	CCGTGGTGTA	GAACAGTCAC	TCCCTGCGCT	CACATCTCCA AGACCCCCCA	GACCACGGCA	GAGGGGACTC	CCCGGGAAGC	
580	640	700	760		880	940	990 1000	1060
AATGGGGACC	CCCATCGTCC	TTCACTTCAG	GCGGCGGACG		CAGTAGCCCA	AGGATGGGCA	CTCCCCCAGC TCTCACTCAG	GGTGTCCCCT
570	630	690	750	800	870	930		1050
TCGCAACGAC	GGCACAGGTG	GAAGAAGTTC	CGGCCTCACT	CCATGAGGAC CACCTTCCTC	GCAGCCGGCC	CGATGGCTGG		ACAGGCCCCT
560	620	680	740	800	860	920	980	1040
CCGAGGGTAC	TGGCAGTCCA	ACAACACCAA	TCCCCACCAG	CCATGAGGAC	GGTCTGGCGT	AGGTGGAAGC	CTCTGTCCGG	GGTCTCAGAC
550	610	670	730	790	850	910	970	1030
TGGATCTATC	GCCTTCTACC	TCCTCCTTCT	CTGGAAGCCA	TGCCACCGGG	GCCACTGCGG	TGGGGAGGGC	CCAAATACCA	TTCTGTCACT

Figure 3C

					AAA
1440	1430	1420	1410	1400	1390
1380 AAAAAAAAA	1360 1370 1380 TCTTGGAAAA AAAAAAAAA	1360 TCTTGGAAAA	1340 1350 CTGTTTTTT ATAAACACAC		1330 TACTCCGTTG
1320 GTCAGCACTG	1300 1310 TGGCCTGAAG AATCTGTGGG		1290 CTGCTCCTGC	1280 TCGGGGCCTG	1270 GAGCCGGGAA
1260 GGGCCACAGG	1250 CACGCACCCT	1240 GTCCCAGACT	1220 1230 GGAGGACCCC GAGGCCAGGA	•	1210 GGAGCAGATG
1200 CGATGGCCCA	1180 1190 GGGCTGAGCC ACAÄGGCCCC	1180 GGGCTGAGCC	1160 1170 rececrere eccecreer	1160 rececrere	1150 AGATGAGGCT
1140 GGGNTGATAA	1120 1130 CCACGCCACC TCTGGGNGCT	1120 CCACGGCACC	1110 GGACTCGCGC	1100 TCGAGGGCAG	1090 CTCCCGGGC

50	Met Glu Leu Trp Pro	•
	GAG Glu	
40	C ATC	
30	AGCGAGCTGGCGCCGCCGCCCGGGCCGGGCC ATG GAG CTG TGG	
20	GCGCCGTCG	
10	GGAGCGAGCTGGCC	

	CTG	9	GCG Ala
	CAG Gln	140	r Cys 7
	GTG	~	TAC Tyr
90	CTG		CTG
	CTG	08	GTC GCC Val Ala 30
	CTG		GTC Val 30
80	CTG		AAG Lys
	TTG		GCC Ala
	CTG	120	TAC
0/	CTG		TTC Phe
	GCG Ala	70	GAG Glu
	GCG	. 10	GCC A Ala
	GCC	(-1	GCG
09	CTG	<u>.</u>	CGC
	TGT	100	AGC

	CTG	Leu	ر الا	2
	CIG			
	TGC	Cys	ì	٠
180	CIC GIC	Val		
	CIC	Leu		
	TCG			
170	ညည	Ala		
	GTG	Val	! !	
	ည္ပ	מ [ע	1	
160	JCC	Val Cor	1	
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	ACG	5	7117	
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į	TGG Trp
230	ATC GGC Ile Gly
	C A1
	ATC Ile
0	AGC Ser
220	G AAC ATG AGC u Asn Met Ser 60
	AAC Asn
	GAG Glu
210	GTG GAG val Glu
	ACG
	CGG
00	66C 61y
	66C 61Y
	CAC His
06	TGC

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		GTG	۷aا 80	Ç	Gic Val	•	ָר ב	Gic Val	110		LIC	Phe		TIC	Phe 140) # -	GAC	Agn	7
	٠	GAG	GIn	320	rer Gre Are Cys Val Ile		ر د د	Glu Glu		410	CTG CTC	Leu Leu			Phe	500	טעט טעע	GIG ALC CCC	D T U
		Trrc	Phe	3	GIC Val		Ę	ATG Met		7				GIC	Val			7 × ×	N N N
	270	ညည	Arg	E	TGT Cys	1	360				GAG	Glu	450	ටුවුව	G1y				
		CIC	Leu	[0 223	GGT CCC Arg Pro		Ç	ATG GGC Met Glv	1	00	AAG CGG	Lys Arg		GGG	G1y	700) () (ATG ACA	Ala Met Thr
		GGG	Gly	310		90				400) 1 1	CTC	Leu	5	יו ב	A.16	Met
	260	TAC	Īγr	(GCC Ala		350	GAC ATG			ATC GCC	Ala	440	ATG TAC	Met Tyr		Ö	AGC ACI' GCC	Ala
ф	•	TTT TAC	Phe		GAG Glu						ATC	Ile		ATG	Met			ACI	Thr
			Tyr	300	CAG			CTG		390		Gln		ATC		,			Ser
Figure 4	0	TTC AAG	Phe Lys 70		CTG	5)]	340	AGC ATC) -		THE GIRE	Val	430	מכב מענ	Gly Leu			TCT	Ser
124	250	TTC	Phe 70	•	AGG) -										130		ည်	Arg
			Ser	290	CCG CGC	5		CAG	5	380	טטט טעט	Arg		ביור <u>י</u>	Val		470	CGG CAG	Arg Gln
		CGA	Arg					CAC	e Tu		ָרָט מיט	Glu		ن	Pro				Arg
	240	GTG	Val		GAC	400	330	AAC	ASII		ָרָ בַּי		7.00	7.7	G1v			AAC	Asn
		TTC GTG	Phe		CGG			TCC AAC CAC C	Jac	270		Leu		ב ב	Leu		460	ATC	Ile
											•							•	

Figure 4C

•				
TAT Tyr 170	AAG Lys	GTC Val 200	AAG Lys	GCC Ala 230
ATC		ATC Ile	680 AAG Lys	GAA Glu
TGG	590 CCT TTT Pro Phe	CCC	ACC Thr	CTG
O () H	ರ ರ	630 GTG Val	AAC	720 GTG Val
AAA Lys	580 AT GGG GAC CTG CT sn Gly Asp Leu Le 180	CAG Gln	670 TTC TAC Phe Tyr 210	CAG Gln
530 GAG AAC CTC Glu Asn Leu	58 GAC ASP 180	GCA	6' TTC Phe 210	GTG (
530 ; AAC ; ASD	666 61y	620 GTC CAG (Val Gln	TCC TCC 'Ser Ser	710 GTC ACA (Val Thr
3 5	& &	დ >	TCC	GTC
AGG	570 GAC	GCA	660 TTC Phe	ACA
520 ATG GTC A Met Val A	AAC Asn	610 TAC CTG Tyr Leu 190	TCT TCC Ser Ser	700 TCA GGA Ser Gly 220
52 ATG Met 160	CGC	67 TAC TYF 190		700 TCA GC Ser G
CGC	560 ACT Thr	TTC	650 GTG TAC Val Tyr	ACT
GAG Glu	GGT G	GCC		TTC
510 GGC Gly	GAG Glu	600 GGC G1y	GTG Val	690 TTC Phe
CTG	550 CCC Pro	AAG Lys	640 CCC Pro	AAG

ridire and	740 750 750 760 770 ACC AGC GGC CTC GCG CTC	o Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val 240	TGC CAC Cys His	250 840 850 860 ACC CCC CAG GAG AAC GGG GCC ACT GCG GGG TCT GGC GTG CAG Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln 270	70 880 890 900 910 920 ICC CAG TAG CCCAGACCACGGCAGGCCATGACCTGGGGAGGGCAGGTGGAAGC
	740 ACC AGC	Thr Ser	TGC CAC C	830 CCC CAG (Pro Gln (cag Tag sln ***
	ပ္ပဲ	Pro '	780 ACC Thr	ACC	8 G &
		11e	GAC ASD	820 AAG Lys	CCG

940 950 960 970 980 CGATGGCTGGAGGGCAGGGGACTCCTCCCGGCTTCCAAATACCACTCTGTCCGG	1000 1010 1020 1030 1040 CTCCCCCAGCTCTCACTCACTCACTCACTCACTCACTCAC
50 BATGGGCAGAGGG	10 1020 rcactcagcccgc 1060 rgtcccctgcagc
940 CGATGGCTGGAGGA	1000 1010 CTCCCCCAGCTCTC 1050 ACAGGCCCCTGGTG
-	

990

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1120 1130 1140 1150 1160	1180 1190 1200 1210 1220	1240 1250 1260 1270 1280	1300 1310 1320 1330 1340	AAAAAA
GGACTCGCGCCCCACGGCACCTCTGGGNGCTGGGNTGATAAAGATGAGGCTTGCGGCTGTG	GCCCGCTGGTGGCCTGAGGCCCCCCGATGGCCCAGGAGGAGGACCCC	GAGGCCAGGAGTCCCAGGCCACACGGGAGCCGGGAATCGGGGCCTG	CTGCTCCTGCTGAAGAATCTGTGGGGTCAGCACTGTACTCCGTTGCTGTTTTTT	
1150	1210	1270	. 1330	aaaaaaaa
SCTGGGNTGA	CCCGATGGC	ccreeccac	segetcaeca	
1140	1200	1260	1320	1380
CCTCTGGGNC	CCACAAGGCO	CTCACGCACO	AGAATCTGT	AAAAAAAA
1130	1190	1250	1310	1360 1370 1380
GCCCACGGCA	Gregecread	GAGTCCCAGA	GCTGGCCTGA	ATAAACACACTCTTGGAAAAAAAAAAAAAAAAAAAAAAA
1120	1180	1240	1300	1360
GGACTCGC	GCCCGCTG	GAGGCCAG	CTGCTCCT	ATAAACAC
1110	1170	1230	1290	1350

Figure 5 A

Alignment of LPAAT Sequences.

10 20 30 40 50 1	51 QL——SRAAE FYAKVALYC ALCTYSAVA SIVCLLCHGG RIVENM-SII 51 TIMFCS BSAK YFFKMAF-YN GWILFTAVLA IPVCAV—RG RNVENM-KIL 51 G——CG—— FY———GVIA SILCTLIGKQ HAQWI-TAR 51 G——MLYI FRLITIVIXS ILVC——VFG SIYCLFSPRN PKHV——ATF 51 ———MLYI FRLITVIXS ILVC——VFG SIYCLFSPRN PKHV——ATF 51 ———MLYI FRLITVIXS ILVC——VFG SIYCLFSPRN PKHV——ATF 51 ———LLSC FKIFVCFAFT VVLITANAWG LIMVLLLPWP YARIRGANA 51 IRWITVILSV VRLAACFL— SMAVITIVM MIMILLLPWP YARIRGANA
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera	Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera

Figure 5 B

151 IPERCVOLAK RELLETIGEV - GLIMYLGGY FEINEGRISST AMT-VMALL 151 ILPGRCV PIAK RELLETIGEV - GLIMYLGGY FEINEGRISST AMT-VMALL 151 ILPGRCV PIAK RELLETIGEV - GLIMYLGGY IFIDRIKRIGD ALS - VMSEV 151 VOPPIVIVGK KSLIMIPFF - GLIMMLICH ILIDRININRIK AHS-TIAEV 151 VOPPIVIVGK KSLIMIPFF TGILYWVICH ILIDRININRIK AHS-TIAEV 151 VOPPIVIVGK KSLIMIPFFF TGILYWVICH ILIDRININRAK AHS-TIAAV 151 VOPPIVIVGK KSLIMIPFFF TGILYWVICH ILIDRININRAK AHS-TIAAV 151 VOPPIVIVGK KSLIMIPFFF TGILYWVICH ILIDRININRAK AHS-TIAAV 151 PROTOVOKK KEVIWYPILG Q-IXTIAHH IRIDRININRAK AHS-TIAAV 151 TPROTOVOK KEVIWYPILG Q-IXTIAHH IRIDRININRAK AHS-TIAAV 151 TPROTOVOK KEVIWYPILG Q-IXTIAHH IRIDRININRAK AHS-TIAAV
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi

Figure 5C

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210 220 230 240 250 201 GERMREINLA WILYPEGTRN DIGIL—LIPF KKGAFTIL—A VQAQVPIVPY 201 LENVKKNKR LIWVFPEGTRS YISELTMLPF KKGAFTIL—A VQAQVPIVPI 201 LENVKKNKR IS IWMFPEGTRS YISELTMLPF KKGAFTIL—A QQGGI PIVPV 201 VNHFKKR IS IWMFPEGTRS RGRGL—LIPF KTGAFTFHAA ISAGVPI IPV 201 VRUTTEKNIS IWMFPEGTRS RGRGL—LIPF KTGAFTFHAA ISAGVPI IPV 201 VRUTTEKNIS LIWFPEGTRS GJGRL—LIPF KTGAFTFHAA IAAGVPI IPV 201 VRUTTEKNIS LIMFPEGTRS GJGRL—LIPF KTGFVHL—A LQSHLPIVPM 201 VRVITTEKNIS LIMFPEGTRS KTGRL—LIPF KKGFVHL—A LQSHLPIVPM 201 VRVITTEKNIS LIMFPEGTRS KTGRL—LIPF KKGFVHL—A LQSHLPIVPM	260 270 280 300 251 VYSSFSSE YNTKKFFTS GTVTVQVLFA IPTSGLTAD VPALVDTCHR 251 VWSNTSTL VSPKYGVFNR GCMTVRLLKE ISTENLITKDK ICEFAEKVRD 251 VCSTTS NK INLARIHN GLVTVEMLPP IDVSG/GKDQ VRELAAHCRP 251 VCSSTH NK INLARIHN GLVTVEMLPP IDVSG/GKDQ VRELAAHCRP 251 VCSSTH NK INLARIHN GLVTVEMLPP IDVSG/GKDQ VRELAAHCRP 251 VCSSTH NK INLARIHN GLVTVEMLPP IDVSG/GKDQ VRELAAHCRP 252 VCSNTS NK VNILARIHN GLVTVEMLPP IDVSG/GKDQ VRELAAHCRP 253 VCSTTLAMF TRYGIFRVRP VPITVKYLPP INTDDMTVLK IDDXVKMIHD 254 VLJCTHLAMF TRYGIFRVRP APITVKYRSP INTDDMTVLK IDDXVKMIHD 255 VLJCTHLAMF TRYGIFRVRP APITVKYRSP INTDDMTVLK IDDXVKMIHD 256 VLJCTHLAMF TRYGIFRVRP APITVKYRSP INTDDMTVLK IDDXVKMIHD 257 VLJCTHLAMF TRYGIFRVRP APITVKYRSP INTDDMTVLK IDDXVKMIHD 258 VVSSTKOFFRVRP APITVKYRSP INTDDMTVLK IDDXVKMIHD 259 VVSSKOFFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 269 VVSSKOFFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 260 VVSSKOFFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 260 VVSSKOFFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 261 VLJCTHLAMF TRYGIFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 261 VLJCTHLAMF TRYGIFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 262 VLJCTHLAMF TRYGIFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 263 VLJCTHLAMF TRYGIFR VRFP APITVKYRSP INTDDMTVLK IDDXVKMIHD 264 VLJCTHLAMF TRYGIFR VRFP APITVKYRSP INTDDMTVK INTDXVKMIHD 265 VLJCTHRAMF TRYGIFR VRFP APITVKYRSP INTDDMTVK INTDXVKMIHD 265 VLJCTHRAMF TRYGIFR VRFP APITVKYRSP INTDDMTVK INTXVKIHD 266 VLJCTHRAMF TRYGIFR VRFP APITVKYRSP INTXVKIHD 267 VLJCTHRAMF TRYGIFR VRFP APITVKYRSP INTXVKIHD 267 VLJCTHRAMF TRYGIFR VRFP APITVKYRSP INTXVKHTHF
MI YPEGTRN DNG DL — L.PF KKGAFHL — A VQAQVPIVPY IWVFPEGTRS YTSEL/IMLPF KKGAFHL — A QQGKI PIVPY IWMFPEGTRS YTSEL/IMLPF KKGAFHL — A QQGKI PIVPY IWMFPEGTRS RGRGL — L.PF KTGAFHL — A QQGKI PIVPY IWMFPEGTRS RGRGL — L.PF KTGAFTFHAA ISAGVPI IPV IWMFPEGTRS RGRGL — L.PF KTGAFTFHAA ISAGVPI IPV LIMFPEGTRS GJGRL — L.PF KKGFVHL — A LQSHLPIVPM LITFPEGTRS KTGRL — L.PF KKGFVHL — A LQSHLPIVPM LITFPEGTRS KTGRL — L.PF KKGFTHFTTA LQTRLPIVPM	YOUNTERFEE GIVIVONLEA IPTSGLEAND VPALADICH VERTERS GOOVRVLEP VPT EGILT POD VPALADRVRH SEPKYSVENR GOMIVRILKE ISTENLITKOK ICEFAEKVRD NK INLARNIN GIVIVEMEP IDVSOKGKDO VRELAAHCRENK INLARNIN GIVIVEMEP VDVSGKKDO VRELAAHCRETRYRIN GIVIVEMEP VDVSGKKDO VRELAAHCRETRYRIN GIVIVEMEP VDVSGKKDO VRELAAHCRETRYRIN GIVIVEMEP INTODMESEK INHYVEMIHE
DNGDL—LPF HNGSM—LPF YTSELIMLPF YTSELIMLPF N RGRGL—LPF S RGRGL—LPF S RGRGL—LPF S RGRGL—LPF S RGRGL—LPF	GIVIVOLEA GOOVRULEA GOMIVELLE GOMIVELEP GENTOEMEP GENTOEMEP GENTOEMEP GENTOEMEP GENTOEMEP
VWI YPEGTRN VWVFPEGTRN LWVFPEGTRS IWMFPEGTRS IWMFPEGTRS LIMFPEGTRS LIMFPEGTRS LIMFPEGTRS LIMFPEGTRS	YNTKKKF FTS YCKK HRRFTS VSPKYGV FNR NK INLANRIHN NK INLANRIHN NK INLANRINN NK YNLANRINN
CEEMARENLK ACTILITOTOR LENVKKNKRA VNHFKKRKIS ARRINEDNIS VRVITEKNIS VRVITEKNIS ARAWKKNIS ARAWKKNIS	VYSS FSSF VWSS YQDF VVS TTS CVS TTS VCSSTH ILTGTHLAW VLTGTHLAW
201 201 201 201 201 201 201 201	251 251 251 251 251 251 251
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera	Human LPAAT-α Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera

Figure 5D

330 340 350 GSGVQPAQ*- KKPGGGG*- PRQAIEYAAL QHDKKVNKKI KNEEVPSVSI EAAGKV*- KGN*- EAAGKV*- KGN*- EATGKV*-	390
310 320 330 301 AMRTTEIHIS KIRDENGATA GSGVQPAQ*- 301 SMLTVEREIS TDGRGGDYL KKPGGGG*- 301 QMVDILKEIG YSPAINDTTL PROAIEYAAL 301 TILMEKRIAE LDKEVA — ER EAAGKV* 301 TALMEQKIAE LDEEIA — — KGN*- 301 TALMEQKIAE LDKEVA — ER EAAGKV* 301 TALMEQKIAE LDKEVA — ER EAAGKV* 301 TALMEQKIAE LDKEVA — ER EATGKV* 301 TALMEQKIAE LDKEVA — ER EATGKV* 301 TALMEQKIAE SQKPLVSKGR DASGRSNS*-	350 370 380 351 351 SAL SAUDANTHANEG SSVKKMH* 351 351 351 351 351 351 351 351
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera	Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera

Figure 9 A

••••••••••••••••••••••••••••••••••••••															
TOTAT GAMACCANCAI TOCK I TOCK													60		
GGC	AGGT	STCTO	GCT	rgtcc	CACCO	:GGA	GCCC	TGAG	GGCA	GCTG	TTCC	CACT	GGCT	CIGC	120 180
TGA	CCTT	GTGC	TTGC	SACGO	CTGT	CCTC	AGCC	AGGG	3CC	CAC	TTC	CICC	CTC	CAGC	225
GCC	ATG	GGC	CTG	CTG	GCC	TTC	CTG	LVC	The	Gln	Phe	Val	Leu	Hie	. 223
					5			-		10					
CTG	CTG	GTC	GGC	TTT	GTC	TTC	GTG	GTG	AGT	GGT	CTG	GTC	ATC	AAC	270
1 5	Leu				20					25					
mmc	GTC	CAG	CTG	TGC	ACG	CTG	GCG	CTC	TGG	CCG	GTC	AGC	AAG	CAG	315
Phe	Val	Gln	Leu	Cys	Thr 35	Leu	Ala	Leu	Trp	40	vai	ser	гĀг	Gin	
ama	ma C	CGC	CGC	CTC	AAC	TGC	CGC	CTC	GCA	TAC	TCA	CTC	TGG	AGC	360
Leu	Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	
4 5	. –				50					22					405
CAA	CTG	GTC	ATG	CTG	CTG	GAG	TGG	TGG	100	TGC	ACG	GAG	CVC	ACA	405
	Leu				65					70					450
CTG	TTC	ACG	GAC	CAG	GCC	ACG	GTA	GAG	CGC	Talat	Clu	AAG	GAG	UAC	450
~ ~ ~	Phe				80					85					405
GCA	GTC	ATC	ATC	CTC	AAC	CAC	AAC	TTC	GAG	ATC	GAC	TTC	CTC	TGT	495
~ ~	Val				95					LUU					
	TGG	ACC	ATG	TGT	GAG	CGC	TTC	GGA	GTG	CTG	GGG	AGC	TCC	AAG	540
	Trp				110					TID					
		GCT	AAG	AAG	GAG	CTG	CTC	TAC	GTG	CCC	CTC	ATC	GGC	TGG	585
Val	Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	PIO	Leu	Ile	Gly	Trp	
120	TGG		mmm.	CMC	125	y ሙብ›	GTG	ጥጥር	TGC	130 AAG	CGG	AAG	TGG	GAG	630
ACG	TGG	TAC	Dhe	T.em	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	
					140					140					675
GAG	GAC	CGG,	GAC	ACC	GTG	GTC	GAA	GGG	CTG	AGG	750	Lou	Ser	GAC	6/3
					155					TOO				Asp	720
TAC	CCC	GAG	TAC	ATG	TGG	TTT	CTC	CTG	TAC	TGC	GAG	GGG	ACC	CGC	720
					170					T/2				Arg	
		GAG	ACC	AAG	CAC	CGC	GTT	AGC	ATG	GAG	GTG	GCG	GCI	GCT	765
Phe	Thr	Glu	Thr	Lys	His	Arg	Val	Ser	mec	190	. vai	AIC	. ATC	. Ala	
		CTT	CCT	GTC	CTC	AAG	TAC	CAC	CTG	CTG	CCG	CGC	ACC	AAG	810
Lys	Gly	Leu	Pro	Val	Leu	Lys	ıyr	HIS	Leu	205	PLU	, wr	, 1111	. Lys	
	_ mmc	ACC	ACC	GCA	GTC	AAG	TGC	CTC	CGG	GGG	ACA	GTC	GC	GCT	855
GIV	Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	GIY	ini	· Val	L Ala	a Ala	
					215					220					000
		GAT	GTA	ACC	CTG	AAC	TTC	AGA	GGA	AAC	AAG	AAC	2 000	TCC	900
Val	Tyr	Asp	Val	Thr	Leu	Asn	Pne	Arg	GIY	235	i păs	, War	1 PI) Ser	
		GGG	ATC	CTC	TAC	GGG	AAG	AAG	TAC	GAG	GCG	GAC	CATO	TGC	945
Lev	Leu	Gly	Ile	Leu	Tyr 245	GIA	Lys	Lys	Туг	: Glu 250	. VIC	. Ası	o Me	Cys	
240)	202	UATALI T	ССФ	ርሞር	GAA	GAC	ATC	CCG			GA	A, AAG	G GAA	990
GTC	AGG ~~~	Ara	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	. Asp	Gli	Ly:	s Glu	
					ったり					203	,			G CTC	
GC	GCT	CAG	166	CI.I.	CAT	~~~	C13			J					

Figure 9 B

Ala	Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu 280	Lys	Asp	Ala	Leu	
270	: - C	አጥል	ጥልጥ	ТАА	275 CAG	AAG	GGC	ATG	TTT	CCA	GGG	GAG	CAG Gln	TTT	1080
Gln	GAG	Tle	Tvr	Asn	Gln	Lys	Gly	Met	Phe	FIU	Gly	Glu	Gln	Phe	
					200					232					1125
AAG	CCT	GCC	CGG	AGG	CCG	TGG	ACC	CTC	CTG	AAC	TTC	CIG	TCC	J.C.C.	1127
Lys	Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	ren	310	Pne	rea	Ser	TTD	
300					305	000	CTC	ጥጥር	AGT		GTC	TTG	GGC	GTC Val	1170
GCC	ACC	ATT	CTC	CTG	TCT	820	Len	Phe	Ser	Phe	Val	Leu	Gly	Val	
Ala					220					343					
315	ccc	AGC	GGA	TCA	CCI	CTC	CTG	ATC	CTG	ACT	TTC	TTG	GGG	TTT	1215
Dhe	Ala.	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	TITT	Fire	Leu	Gly	Phe	
					776					340					1260
	GGA	GCA	GCT	TCC	TTT	GGA	GTT	CGC	AGA	CIG	Tle	. GGA	. Val	ACT	
Val	Gly	Ala	Ala	Ser	Phe	GIY	vaı	Arg	ALG	355	. 116	. 013	,	Thr	
345				ccc	350	AGC	TAC	GGA	AAC	CAA	GAG	TTI	AAG	AAA Lvs	1305
GAG	ATA	GAA	TAKE	Glv	Ser	Ser	Tyr	Gly	Asn	Glr	ı Glu	Phe	Lys	Lys	
															1362
AAG	GAA	TAA	TTA	ATGG	CTGT	GACT	GAAC	ACAC	GCGG	CCCI	rgaco	GTGC	TATC	CAGTT	. 1302
															1422
														TATTAA STCAGG SGGAGG	1482
															1542
				3000	-	יריברינ.	TALL			ι					1602
CC)	CCTT	TGGC	TGCI	TTCI	CTCC	TTAP	ACT	ragar	CAA	TTT.	AAAT	AAAA	AAAA	AAAA	1660

Figure 10 A

													61		
TO CHOOK CHOTEGACOCTAGOACAAAACTAGAAGCAACCCAAGCACCTGTCACTGGAGACT													121		
AATTATGCGGCACCCATACAGGGACCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC CGTACAGTTTTAAGCGAAAAAGGAAGTATACAACAAAAGTCCATAACTGGTC ATG CTG													181		
AATI	<u> </u>	rana i	AGCC	ZAAAZ	AGGA	AGTA	TACA	ACAA	AGTC	CATA	ACTG	GTC	ATG	CTG	238
CGTF	CAG		<u> </u>								- .		Met	Leu	
															~
		mcc.	mcc.	TCC	TCC	ACG	GAG	ፐር ፐ	ACA	CTG	TTC	ACG	GAC	CAG	283
CTG	GAG	166	166	700	Cura	WP~	Glu	Cve	Thr	Leu	Phe	Thr	ASD	Gln	
Leu	Glu		Trp	Ser	CAS	1111	10	Cys	* ***			15			
		5				000		CAG	CAC	CCA	CTC		ልጥሮ	CTC	328
GCC	ACG	GTA	GAG	CGC	L'I'I	C1	TAG	Clu	CAC	Ala	Val	Tle	Tle	T.eu	220
Ala	Thr		GIu	Arg	Fue	GIĀ	25	GIU	His	A10	V G I	30	116	Dea	
		20				636		CTC	ጥርጥ	GGG	TCC		ATTC	υCιτ.	373
AAC	CAC	AAC	TTC	GAG	ATC	GAC	TIC.	CIC	TGT	Clv	TGG	Th-	Mot	Cvc	3,3
Asn	His		Phe	Glu	IIe	Asp	Pne	rea	Cys	Gry	TTD	45	Mec	Cys	
		35					40	mcc	220	CEC	CTC		N N C	אמ	418
GAG	CGC	TTC	GGA	GTG	CTG	GGG	AGC	TCC	AAG	Wal.	LOU	712	LVC	Tyc	410
Glu	Arg		Gly	Val	Leu	GIA	Ser	ser	Lys	AGT	Leu	60	Lys	nys	
		50					55		mcc.	3.00	mcc.		TVT TV	CTC	463
GAG	CTG	CTC	TAC	GTG	CCC	CTC	ATC	Clar	TGG	WCG	TGG	TAC	Dho	LOU	402
Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	GIY	Trp	Thr	Trp	75	Pne	Leu	
		65					70	mac	030	CNC	CXC		CAC	3 CC	508
GAG	TTA	GTG	TTC	TGC	AAG	CGG	AAG	166	GAG	GAG	GAC	200	3AC	MCC	308
Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	GIU	Asp	Arg	Asp	THE	
		80	•				85			ma 0	000	90	m».c	3.000	
GTG	GTC	GAA	GGG	CTG	AGG	CGC	CTG	TCG	GAC	TAC	000	GAG	TAC	ATG	553
Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	JĀL	PIO	105	TYL	Met	
		95					100					105		220	500
TGG	TTT	CTC	CTG	TAC	TGC	GAG	GGG	ACG	CGC	TTC	ACG	GAG	ACC	AAG	598
Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Pne	THE	GIU	THE	Lys	
		11 A					112					120			643
CAC	CGC	GTT	AGC	ATG	GAG	GTG	GCG	GCT.	GCT	AAG	666	CTT	D	GTC	. 643
His	Arg	Val	Ser	Met	Glu	Val	Ala	AIA	ALA	Lys	GIA	Leu	PIO	Val	
		125					130			~~~	mma	135		CCN	688
CTC	AAG	TAC	CAC	CTG	CTG	CCG	CGG	ACC	AAG	GGC	TITC	MCC.	ML-	GCA	000
Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	rys	GIA	Pne	THE	The	Ala	
		140					145				~ ~ ~	150		3.00	733
GTC	AAG	TGC	CTC	CGG	GGG	ACA	GTC	GCA	GCT.	GIC	TAT	GAT	. U.S	ACC	133
Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	val	TAL	ASE	, val	Thr	
		165					160					TOS	,		770
CTG	AAC	TTC	AGA	GGA	AAC	AAG	AAC	CCG	TCC	CIG	CIG	GGG	ATC	CTC	778
Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	Leu	GTZ	116	Leu	
		170					175					TOI	,	•	023
TAC	GGG	AAG	AAG	TAC	GAG	GCG	GAC	ATG	TGC	GIG	AGG	AG	. J.T.	CCT	823
TVI	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	Arg	AF	j Pne	e Pro	
		105					TAA						,		0.00
CTG	GAA	GAC	ATC	CCG	CTG	GAT	GAA	AAG	GAA	GCA	GCT	CAC	3 TGC	CTT	868
T.eu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	гĀг	Glu	Ala	Ala	GII	I III) Leu	
		200					705					21	,		
T_{A}	AAA	CTG	TAC	CAG	GAG	AAG	GAC	GCG	CTC	CAG	GAG	AT	A TA	TAA T	913
uie	Lvs	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	ı Glu	1 11	E TA.	r Asn	
		215					220					~~.	,		
CAC	n n G	CCC	ATG	TTT	CCA	GGG	GAG	CAG	TTI	' AAG	CCI	GC	C CG	G AGG	958
CAG	Luc	Glv	Met	Phe	Pro	Glv	Glu	Gln	Phe	Lys	Pro	Ala	a Ar	g Arg	
		220										2 4	•		
	mcc.	100	רתכ	CTG	AAC	TTC	CTG	TCC	TGG	GCC	ACC	: AT	r cr	CTG	1003
CCC	1.00	Mr-	Leu	T.e.	Acn	Phe	Leu	Ser	Trp	Ala	Thr	: Il	e Le	u Leu	
		~46					270						_		
		.245	The Co	ልርጥ	July	GTC	ጥጥር	GGC	GTC	TTI	GCC	: AG	c GG	A TCA	1048
TCT	CCC	CIC	DF-	201	Dho	Va 1	Len	Glv	Val	Phe	Ala	Se	r Gl	y Ser	
Ser	Pro	Leu	rne	ser	FIIG	A G T		3					_ .		

Figure 10 B

												270			
		260					265					270			
CCT	CTC	CTG	ATC	CTG	ACT	TTC	TTG	GGG	TTT	GTG	GGA	GCA	GCT	TCC	1093
Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	Gly	Ala	Ala	Ser	
		275					280					285			
்மமுமு	GGA	GTT	CGC	AGA	CTG	ATA	GGA	GTA	ACT	GAG	ATA	GAA	AAA	GGC	1138
Dhe	Gly	Val	Arg	Arq	Leu	Ile	Gly	Val	Thr	Glu	Ile	Glu	Lys	Gly	
	_	290					295					300			
TCC	AGC	TAC	GGA	AAC	CAA	GAG	TTT	AAG	AAA	AAG	GAA	TAA	TTA	ATGGC	1185
200	Ser	ጥህዮ	Glv	Asn	Gln	Glu	Phe	Lys	Lys	Lys	Glu	***			
261	Ser	305	.0-1				310	_	_			•			
mcm	- x - m/	בטכ יסממי	ACAC	ברככנ	ירריוים	SACGO	TGG	PATC	CAGT"	TAAC'	TCAA	AACC.	AACA	CACAC	1245
TGT	SACIC						יחיוויייייייייייייייייייייייייייייייייי	יייים אייים אייים	ልጥጥል	ACTC	CTCA	מ בידי	ጥልጥጥ	AACAA	1305
AGT	GCAG	SAAA	AGAC	JAI.IA	AGAA	ACTA:	1111	10111	7117	200	0100				1303
AAC	TTGA	CCA	AGAG:	PAAA 1	GAAT'	rcag?	AAGG	CTG'	rcag	GTGA	AGTC	TTCA	GCCT	CCCAC	1365
3.00	CCNCC	CTC	CAGO	ATC	CCA	CGCG		CGTG	GGAG(GTGG	GTCC	GGCC	GGAG.	AGGCC	1425
AGC	CAG	3010		-mm-		እ አ ሮጥ(הערכר:	AAGA	GGGA	CCTT	TGGC	TGCT	TTCTC	1485
TCC	CGCG	SACG	-CGT	-1-1	LUAGA	4VC 1									1523
TCC	TTAAI	ACTT	AGAT	CAAA!	TTTT	AAAA	AAAA	AAAA	AAA						1343

Figure 11A

, .gu.								•							_
TCA ACCCAGCICCATCICAGCIICIGGII												61			
- TO CC	2020	CCCI	ኮጥርርፕ	CAGT	'CCTG	GATC	TTTC	TTCC	TICI	GGAP	TALCI.	TIGA	CTGT	GGG	121 · 175
TAGTI	ATTI	TTTA!	CTGA	ATAA	GAGC	GTCC	ACGC	ATC	MAL	Aen	LAU	0CG	GGA (Gly :	Lau	1/3
									Hec	rap	Dea	vra	Gry .	Deu	
	3 3 C	TCT	CAG	ጥጥር	CTG	TGC	CAC	CTG	GTC	TTC	TGC	TAC	GTC '	TTT	220
CIG	LAG	Ser	Gln	Phe	Leu	Cvs	His	Leu	Val	Phe	Cys .	Tyr	Val	Phe	
	_		10					15					20		
ATT	GCC	TCA	GGG	CTA	ATC	ATC	AAC	ACC	TTA	CAG	CTC	TTC	ACT	CTC	265
Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	Ile	Gln	Leu	Phe	Thr	Leu	
			25					30					35		310
CTC	CTC	TGG	CCC	TTA	AAC	AAG	CAG	CTC	Dhe	7.CG	Tare	TIO	AAC	Cue	310
Leu	Leu	Trp		IIe	ASI	гĀг	GIII	Leu 45	FIIC	AL 9	Lys	TIE	50	Cys	
	CITIC .	mcc	40 Tar	TCC	אייר	тса	AGC	CAG	CTG	GTG	ATG	CTG	CTG	GAG	355
AGA	T.ell	Ser	TVT	Cvs	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu	Leu	Glu	ŕ
_			55					60					65		
TGG	TGG	TCG	GGC	ACG	GAA	TGC	ACC	ATC	TTC	ACG	GAC	CCG	CGC	GCC	400
Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg	Ala	
			70			C 2 2	አልሞ	GCC	ልጥሮ	GTG	CTT	CTC	80	CAC	445
TAC	CTC	AAG	TAT	GGG	AAG	GAA	AAI	Ala	Ile	Val	Val	Leu	Asn	His	445
-			. 0 5					.90					95		
AAG	արդ	GAA	ערעה ע	GAC	TTT	CTG	TGT	GGC	TGG	AGC	CTG	TCC	GAA	CGC	490
LVS	Phe	Glu	Ile	Asp	Phe	Leu	Cys	GIĀ	Trp	Ser	Leu	Ser	GIA	Arg	
-			100					105					TIU		525
TTT	GGG	CTG	TTA	GGG	GGC	TCC	AAG	GTC	CIG	Ala	AAG	AAA	Clu	Lou	535
Phe	Gly	Leu		GIĀ	GIY	Ser	Lys	Val 120	Dea	ATO	. Lys	БŽЗ	125	Dea	
	m a m	CTC	115	איים ע	ልጥር	GGC	TGG	ATG	TGG	TAC	TTC	ACC	GAG	ATG	580
81 a	TWI	Val	Pro	Ile	Ile	Gly	Trp	Met	Trp	Туг	Phe	Thr	Glu	Met	
			120					TID					140		
GTC	TTC	TGT	TCG	CGC	AAG	TGG	GAG	CAG	GAT	CGC	AAG	ACG	GTT	GCC	625
Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln 150	Asp	Arg	1 Lys	Thr	Val 155	Ala	
			145		ama	ccc	GAC	TAC	CCC	GAC		י דאַ	להלהלה בכד	ጥጥር	670
ACC	AGT	TTG	CAG	CAC	Len	Ara	Asp	Tyr	Pro	Glu	Lys	Tyr	Phe	Phe	
			160					TPD					T/0		
CTG	ጉጥ	CAC	m-m	GAG	GGC	ACA	CGG	TTC	ACG	GAG	G AAC	AAG	CAT	GAG	715
Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	Pne	THE	Gl	ı Lys	: Lys	HIS	GIU	
			175					TAA					T03)	760
ATC	AGC	ATG	CAG	GTG	GCC	CGG	GCC	TAG	GUG	, C10	Dro	Arc	. Crc	AAG Lys	700
Ile	Ser	Met	Gln	Val	Ala	Arg	MIG	195	Gly	De		, 44.6	200	, bys	
	010	CTC	190	CCA	CGA	ACC	AAG	GGC	TTC	: GC	CATO	ACC	GTG	AGG	805
CAT	CAC	Lau	T.en	Pro	Ara	Thr	Lys	Gly	Phe	Ala	a Ile	Thi	. Val	Arg	
			205					210	,				213)	
AGC	тTG	AGA	220	CTA	GTT	TCA	GCI	GT.	LAT .	GA	C TG:	r ac	A CTC	AAT	850
Ser	Leu	Arg	Asn	Val	Val	Ser	Ala	l vai	. TYI	As	р Су:	s Thi	r Let	ı Asn	
			220					. 243)				23	,	905
TTC	AGA	AAT	' AAT	GAA	AAT	CCA	ACA	CTC	CTC	نای د	A GT	CTA	A AAC	GGA	895
Phe	Arg	Asn	Asn	Glu	Asn	Pro	LUI	240	י הפו	. 61	y Vd.	י הפו	1 ASI 249	Gly	
			235	do:	~ » ~	THE C	ጥልጥ			AC	G ልጥ	ב ככי			940
AAG	AAA	TAC	CAT	GCA	BAT	יום.	ጥ ተጥ ተ	Val	Arc	Ar	g Ile	e Pro	Lei	GAA Glu	
			っちん					232	1			-	201	,	
010	7 mc	CCT	C 2 2	GAC	GAT	GAC	GAG	TGC	TCC	GC	C TG	G CT	G CAC	AAG	985
GAC 3 co	TIP	Pro	Glu	Asp	Asp	Asp	Glu	Cys	s sei	c Al	a Tr	p Le	n ur:	s razi	
vah			265		•	_		270)				279	5	

Figure 11B

CTC TAC CAG GAG	AAG GAT	GCC 1	rtt (CAG	GAG	GAG	TAC	TAC	AGG	ACG	1030
Leu Tyr Gln Glu	Lys Asp	Ala P	Phe C	Gln	Glu	Glu	Tyr	Tyr	Arg	Thr	
. 280				285					290		
GGC ACC TTC CCA	GAG ACG	CCC 2	ATG (GTG	CCC	CCC	CGG	CGG	CCC	TGG	1075
Gly Thr Phe Pro	Glu Thr	Pro 1	Met \	Val	Pro	Pro	Arg	Arg	Pro	Trp	
295				300					305		
ACC CTC GTG AAC	TGG CTG	TTT	TGG (GCC	TCG	CTG	GTG	CTC	TAC	CCT	1120
Thr Leu Val Asn		Phe ?	Trp	Ala	Ser	Leu	Val	Leu	JAT	PIO	_
. 310				315		100		mem	320	CITYC	1165
TTC TTC CAG TTC	CTG GTC	AGC	ATG .	ATC	AGG	AGC	Clar	COT	502	Lou	1103
Phe Phe Gln Phe		Ser	met .	330	Arg	Ser	GIĀ	SET	335	nea	
325 ACG CTG GCC AGC					עזארע	GTG	GCC	TCC		GGA	1210
ACG CTG GCC AGC Thr Leu Ala Ser	Pho Ile	T.en	Val	Phe	Phe	Val	Ala	Ser	Val		
Thr Leu Ala Sel		Dea	142	345					350		
COM CCA MCG ATG	רסט ידיים	GTG	ACG	GAA	ATT	GAC	AAG	GGC	TCT	GCC	1255
Val Arg Trp Met	Ile Gly	Val	Thr	Glu	Ile	Asp	Lys	Gly	Ser	Ala	366
355				360					365		•
TAC GGC AAC TCT	GAC AGO	AAG	CAG	AAA	CTG	TAA	GAC	TGA	CTC	AGGG	1301
Tyr Gly Asn Ser	Asp Ser	Lys	Gln	Lys	Leu	Asn	Asp	***			
370				375						ma cm	1361
AGGTGTCACCATCCGA	AGGGAACC	TTGGG	GAAC	TGG:	rggc	CTCT	GCAT	CEC	CCAC	CTCT	1421
GGGACACGGTGACAAA CCAGCCAGGGAGTCTG	GGCTGGG1	GAGCC	CCTG	CIG(SGCA1	CATC	ᡴᠬᠬᠳ	CTL	ערטאכי יירטייי	deletate CTCT	1481
CCAGCCAGGGAGTCTG TCCCCATGTGCTTTAG	GTCTCAAG	CCTTT	ATGG	᠁ᢕᡗ	こかんかい	CACT	CTCT	CTGA	GAAT	GGCT	1541
TCCCCATGTGCTTAG GTGTGGTGAGTGTGAA	. L. G. G. G. C. L. T. 1	יתכתיה מביתבתי	TCIT	AGA	AAGG	GTAT	TTTA	GGCI	GCAG	GGGA	1601
	CCAAGGGG	CACAG	TTCC	CCT	ГТСА	TCCI	TTGG	TGC	GAGI	"I"I"I"C	1661
TOTAL ACCOMPAGE TEST	CAGAGATI	LAAGTG	AAAA	GTG	$\mathtt{T}\mathtt{T}\mathtt{T}\mathtt{T}$	AGG'I	'GAGP	TGAC	TAA	TATT	1721
GCCTCCAAGAAAAAA	AATTAAA	TGCTT	TTCT	'GGG	TCAA	AAAA	AAA A	LAAA	\A		1774